

SEQUENCE LISTING

<110> Kennedy, Giulia C.

<120> Polynucleotides Differentially Expressed
in Adenocarcinomas, Polypeptides Encoded Thereby, and
Methods of Use Thereof

<130> 2300-1575

<150> 60/145,612

<151> 1999-07-26

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<151> 1999-08-13

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tct gga gaa ggg gaa atc tcc cca caa aga gaa gtc tca aga tcc cag Ser Gly Glu Gly Ile Ser Pro Gln Arg Glu Val Ser Arg Ser Gln	395	400	405	1915	
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gat tca aaa gag tgg gag gaa gcc atg gct aag gct caa gaa act gga Asp Ser Lys Glu Trp Glu Glu Ala Met Ala Lys Ala Gln Glu Thr Gly	475	480	485		2155
cac cta gtg atg gat gtg agg cgc tat gga aag gct ggt tca cct gaa His Leu Val Met Asp Val Arg Arg Tyr Gly Lys Ala Gly Ser Pro Glu	490	495	500		2203
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tca aat cta tct gta aca act gat ttc tcc gaa agc ctt cag agt tct Ser Asn Leu Ser Val Thr Asp Phe Ser Glu Ser Leu Gln Ser Ser	520	525	530		2299
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Asn Ser Trp Ile Arg Gln Arg Ser Ala Ser Val Asn Lys Glu Pro Val			
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Ser Leu Pro Gly Ile Met Arg Arg Gly Glu Ser Leu Asp Asn Leu Asp			
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Arg Ile Arg Asn His Gln Leu Tyr Cys Asn Asp Cys Tyr Leu Arg Phe			
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 Glu Ala Asp Gly Thr Phe Ser Arg Ser Lys Ser Met Ser Asp Val Ser
 65 70 75 80
 Ala Glu Asp Val Gln Asn Leu Arg Gln Leu Arg Tyr Glu Glu Met Gln
 85 90 95
 Lys Ile Lys Ser Gln Leu Lys Glu Gln Asp Gln Lys Trp Gln Asp Asp
 100 105 110
 Leu Ala Lys Trp Lys Asp Arg Arg Lys Ser Tyr Thr Ser Asp Leu Gln
 115 120 125
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Val	Thr	Thr
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Pro	Ala	Ser
Leu	Ser	Ser
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Ser	Thr	Arg
Val	Ser	Ala
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Arg	Thr	Val
Leu	Thr	Ser
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Ile	Ser	Ser
Leu	Pro	Arg
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Trp	Lys	Tyr
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Arg	Leu	Pro
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Thr	Pro	Gly
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Glu	Lys	Ser
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Val Pro Ala Pro Leu Arg Lys Lys Pro Asp Lys His Glu Asp Asn						
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75	80	85				
agt gat gtc agc gca gaa gat gtt caa aac ttg cgt cag ctg cgt tac						1003
Ser Asp Val Ser Ala Glu Asp Val Gln Asn Leu Arg Gln Leu Arg Tyr						

90	95	100	
gag gag atg cag aaa ata aaa tca caa tta aaa gaa caa gat cag aaa Glu Glu Met Gln Lys Ile Lys Ser Gln Leu Lys Glu Gln Asp Gln Lys 105	110	115	1051
tgg cag gat gac ctt gca aaa tgg aaa gat cgt cga aaa agt tac act Trp Gln Asp Asp Leu Ala Lys Trp Lys Asp Arg Arg Lys Ser Tyr Thr 120	125	130	1099
tca gat ctg cag aag aaa aaa gaa gag aga gaa att gaa aag cag Ser Asp Leu Gln Lys Lys Glu Glu Arg Glu Glu Ile Glu Lys Gln 135	140	145	1147
gca ctt gag aag tct aag aga agc tct aag acg ttt aag gaa atg ctg Ala Leu Glu Lys Ser Lys Arg Ser Ser Lys Thr Phe Lys Glu Met Leu 155	160	165	1195
cag gac agg gaa tcc caa aat caa aag tct aca gtt ccg tca aga agg Gln Asp Arg Glu Ser Gln Asn Gln Lys Ser Thr Val Pro Ser Arg Arg 170	175	180	1243
aga atg tat tct ttt gat gat gtg ctg gag gaa gga aag cga ccc cct Arg Met Tyr Ser Phe Asp Asp Val Leu Glu Glu Gly Lys Arg Pro Pro 185	190	195	1291
aca atg act gtg tca gaa gca agt tac cag agt gag aga gta gaa gag Thr Met Thr Val Ser Glu Ala Ser Tyr Gln Ser Glu Arg Val Glu Glu 200	205	210	1339
aag gga gca act tat cct tca gaa att ccc aaa gaa gat tct acc act Lys Gly Ala Thr Tyr Pro Ser Glu Ile Pro Lys Glu Asp Ser Thr Thr 215	220	225	1387
ttt gca aaa aga gag gac cgt gta aca act gaa att cag ctt cct tct Phe Ala Lys Arg Glu Asp Arg Val Thr Thr Glu Ile Gln Leu Pro Ser 235	240	245	1435
caa agt cct gtg gaa gaa caa agc cca gcc tct ttg tct tct ctg cgt Gln Ser Pro Val Glu Glu Gln Ser Pro Ala Ser Leu Ser Ser Leu Arg 250	255	260	1483
tca cgg agc aca caa atg gaa tca act cgt gtt tca gct tct ctc ccc Ser Arg Ser Thr Gln Met Glu Ser Thr Arg Val Ser Ala Ser Leu Pro 265	270	275	1531
aga agt tac cgg aaa act gat aca gtc agg tta aca tct gtg gtc aca Arg Ser Tyr Arg Lys Thr Asp Thr Val Arg Leu Thr Ser Val Val Thr 280	285	290	1579
cca aga ccc ttt ggc tct cag aca agg gga atc tca tca ctc ccc aga			1627

Pro Arg Pro Phe Gly Ser Gln Thr Arg Gly Ile Ser Ser Leu Pro Arg			
295	300	305	310
tct tac acg atg gat gat gct tgg aag tat aat gga gat gtt gaa gac			1675
Ser Tyr Thr Met Asp Asp Ala Trp Lys Tyr Asn Gly Asp Val Glu Asp			
315	320	325	
att aag aga act cca aac aat gtg gtc agc acc cct gca cca agc ccg			1723
Ile Lys Arg Thr Pro Asn Asn Val Val Ser Thr Pro Ala Pro Ser Pro			
330	335	340	
gac gca agc caa ctg gct tca agc tta tct agc cag aaa gag gta gca			1771
Asp Ala Ser Gln Leu Ala Ser Ser Leu Ser Ser Gln Lys Glu Val Ala			
345	350	355	
gca aca gaa gaa gat gtg aca agg ctg ccc tct cct aca tcc ccc ttc			1819
Ala Thr Glu Glu Asp Val Thr Arg Leu Pro Ser Pro Thr Ser Pro Phe			
360	365	370	
tca tct ctt tcc caa gac cag gct gcc act tct aaa gcc aca ttg tct			1867
Ser Ser Leu Ser Gln Asp Gln Ala Ala Thr Ser Lys Ala Thr Leu Ser			
375	380	385	390
tcc aca tct ggt ctt gat tta atg tct gaa tct gga gaa ggg gaa atc			1915
Ser Thr Ser Gly Leu Asp Leu Met Ser Glu Ser Gly Glu Gly Glu Ile			
395	400	405	
tcc cca caa aga gaa gtc tca aga tcc cag gat cag ttc agt gat atg			1963
Ser Pro Gln Arg Glu Val Ser Arg Ser Gln Asp Gln Phe Ser Asp Met			
410	415	420	
aga atc agc ata aac cag acg cct ggg aag agt ctt gac ttt ggg ttt			2011
Arg Ile Ser Ile Asn Gln Thr Pro Gly Lys Ser Leu Asp Phe Gly Phe			
425	430	435	
aca ata aaa tgg gat att cct ggg atc ttc gta gca tca gtt gaa gca			2059
Thr Ile Lys Trp Asp Ile Pro Gly Ile Phe Val Ala Ser Val Glu Ala			
440	445	450	
ggt agc cca gca gaa ttt tct cag cta caa gta gat gat gaa att att			2107
Gly Ser Pro Ala Glu Phe Ser Gln Leu Gln Val Asp Asp Glu Ile Ile			
455	460	465	470
gct att aac aac acc aag ttt tca tat aac gat tca aaa gag tgg gag			2155
Ala Ile Asn Asn Thr Lys Phe Ser Tyr Asn Asp Ser Lys Glu Trp Glu			
475	480	485	
gaa gcc atg gct aag gct caa gaa act gga cac cta gtg atg gat gtg			2203
Glu Ala Met Ala Lys Ala Gln Glu Thr Gly His Leu Val Met Asp Val			
490	495	500	

agg cgc tat gga aag gct ggt tca cct gaa aca aag tgg att gat gca Arg Arg Tyr Gly Lys Ala Gly Ser Pro Glu Thr Lys Trp Ile Asp Ala	505	510	515	2251
act tct gga att tac aac tca gaa aaa tct tca aat cta tct gta aca Thr Ser Gly Ile Tyr Asn Ser Glu Lys Ser Ser Asn Leu Ser Val Thr	520	525	530	2299
act gat ttc tcc gaa agc ctt cag agt tct aat att gaa tcc aaa gaa Thr Asp Phe Ser Glu Ser Leu Gln Ser Ser Asn Ile Glu Ser Lys Glu	535	540	545	2347
atc aat gga att cat gat gaa agc aat gct ttt gaa tca aaa gca tct Ile Asn Gly Ile His Asp Glu Ser Asn Ala Phe Glu Ser Lys Ala Ser	555	560	565	2395
gaa tcc att tct ttg aaa aac tta aaa agg cga tca caa ttt ttt gaa Glu Ser Ile Ser Leu Lys Asn Leu Lys Arg Arg Ser Gln Phe Phe Glu	570	575	580	2443
caa gga agc tct gat tcg gtg gtt cct gat ctt cca gtt cca acc atc Gln Gly Ser Ser Asp Ser Val Val Pro Asp Leu Pro Val Pro Thr Ile	585	590	595	2491
agt gcc ccg agt cgc tgg gtg tgg gat caa gag gag gag cg ^g aag cg ^g Ser Ala Pro Ser Arg Trp Val Trp Asp Gln Glu Glu Arg Lys Arg	600	605	610	2539
cag gag agg tgg cag aag gag cag gac cgc cta ctg cag gaa aaa tat Gln Glu Arg Trp Gln Lys Glu Gln Asp Arg Leu Leu Gln Glu Lys Tyr	615	620	625	2587
caa cgt gag cag gag aaa ctg agg gaa gag tgg caa agg gcc aaa cag Gln Arg Glu Gln Glu Lys Leu Arg Glu Trp Gln Arg Ala Lys Gln	635	640	645	2635
gag gca gag aga gag aat tcc aag tac ttg gat gag gaa ctg atg gtc Glu Ala Glu Arg Glu Asn Ser Lys Tyr Leu Asp Glu Glu Leu Met Val	650	655	660	2683
cta agc tca aac agc atg tct ctg acc aca cg ^g gag ccc tct ctt gcc Leu Ser Ser Asn Ser Met Ser Leu Thr Thr Arg Glu Pro Ser Leu Ala	665	670	675	2731
acc tgg gaa gct acc tgg agt gaa ggg tcc aag tct tca gac aga gaa Thr Trp Glu Ala Thr Trp Ser Glu Gly Ser Lys Ser Ser Asp Arg Glu	680	685	690	2779
gga acc cga gca gga gaa gag gag agg aga cag cca caa gag gaa gtt Gly Thr Arg Ala Gly Glu Glu Arg Arg Gln Pro Gln Glu Glu Val	695	700	705	710

gtt cat gag gac caa gga aag aag ccg cag gat cag ctt gtt att gag Val His Glu Asp Gln Gly Lys Lys Pro Gln Asp Gln Leu Val Ile Glu 715	720	725	2875
aga gag agg aaa tgg gag caa cag ctt cag gaa gag caa gag caa aag Arg Glu Arg Lys Trp Glu Gln Gln Leu Gln Glu Glu Gln Glu Gln Lys 730	735	740	2923
cgg ctt cag gct gag gag cag aag cgt cct gcg gag gag cag Arg Leu Gln Ala Glu Ala Glu Glu Gln Lys Arg Pro Ala Glu Glu Gln 745	750	755	2971
aag cgc cag gca gag ata gag cgg gaa aca tca gtc aga ata tac cag Lys Arg Gln Ala Glu Ile Glu Arg Glu Thr Ser Val Arg Ile Tyr Gln 760	765	770	3019
tac agg agg cct gtt gat tcc tat gat ata cca aag aca gaa gca Tyr Arg Arg Pro Val Asp Ser Tyr Asp Ile Pro Lys Thr Glu Glu Ala 775	780	785	3067
790			
tct tca ggt ttt ctt cct ggt gac agg aat aaa tcc aga tct act act Ser Ser Gly Phe Leu Pro Gly Asp Arg Asn Lys Ser Arg Ser Thr Thr 795	800	805	3115
gaa ctg gat gat tac tcc aca aat aaa aat gga aac aat aaa tat tta Glu Leu Asp Asp Tyr Ser Thr Asn Lys Asn Gly Asn Asn Lys Tyr Leu 810	815	820	3163
gac caa att ggg aac acg acc tct tca cag agg aga tcc aag aaa gaa Asp Gln Ile Gly Asn Thr Ser Ser Gln Arg Arg Ser Lys Lys Glu 825	830	835	3211
caa gta cca tca gga gca gaa ttg gag agg caa caa atc ctt cag gaa Gln Val Pro Ser Gly Ala Glu Leu Glu Arg Gln Ile Leu Gln Glu 840	845	850	3259
atg agg aag aga aca ccc ctt cac aat gac aac agc tgg atc cga cag Met Arg Lys Arg Thr Pro Leu His Asn Asp Asn Ser Trp Ile Arg Gln 855	860	865	3307
870			
cgc agt gcc agt gtc aac aaa gag cct gtt agt ctt cct ggg atc atg Arg Ser Ala Ser Val Asn Lys Glu Pro Val Ser Leu Pro Gly Ile Met 875	880	885	3355
aga aga ggc gaa tct tta gat aac ctg gac tcc ccc cga tcc aat tct Arg Arg Gly Glu Ser Leu Asp Asn Leu Asp Ser Pro Arg Ser Asn Ser 890	895	900	3403
tgg aga cag cct cct tgg ctc aat cag ccc aca gga ttc tat gct tct Trp Arg Gln Pro Pro Trp Leu Asn Gln Pro Thr Gly Phe Tyr Ala Ser 915	920	925	3451

905	910	915	
tcc tct gtg caa gac ttt agt cgc cca cca cct cag ctg gtg tcc aca Ser Ser Val Gln Asp Phe Ser Arg Pro Pro Pro Gln Leu Val Ser Thr 920.	925	930	3499
tca aac cgt gcc tac atg cg ^g aac ccc tcc tcc agc gtg ccc cca cct Ser Asn Arg Ala Tyr Met Arg Asn Pro Ser Ser Ser Val Pro Pro Pro 935 940 945 950			3547
tca gct ggc tcc gtg aag acc tcc acc aca ggt gtg gcc acc aca cag Ser Ala Gly Ser Val Lys Thr Ser Thr Thr Gly Val Ala Thr Thr Gln 955 960 965			3595
tcc ccc acc ccg aga agc cat tcc cct tca gct tca cag tca ggc tct Ser Pro Thr Pro Arg Ser His Ser Pro Ser Ala Ser Gln Ser Gly Ser 970 975 980			3643
cag ctg cgt aac agg tca gtc agt ggg aag cgc ata tgc tcc tac tgc Gln Leu Arg Asn Arg Ser Val Ser Gly Lys Arg Ile Cys Ser Tyr Cys 985 990 995			3691
aat aac att ctg ggc aaa gga gcc gcc atg atc atc gag tcc ctg ggt Asn Asn Ile Leu Gly Lys Gly Ala Ala Met Ile Ile Glu Ser Leu Gly 1000 1005 1010			3739
ctt tgt tat cat ttg cat tgt ttt aag tgt gtt gcc tgt gag tgt gac Leu Cys Tyr His Leu His Cys Phe Lys Cys Val Ala Cys Glu Cys Asp 1015 1020 1025 1030			3787
ctc gga ggc tct tcc tca gga gct gaa gtc agg atc aga aac cac caa Leu Gly Gly Ser Ser Ser Gly Ala Glu Val Arg Ile Arg Asn His Gln 1035 1040 1045			3835
ctg tac tgc aac gac tgc tat ctc aga ttc aaa tct gga cgg cca acc Leu Tyr Cys Asn Asp Cys Tyr Leu Arg Phe Lys Ser Gly Arg Pro Thr 1050 1055 1060			3883
gcc atg tga tgtaaggc ^c tc catacgaaag cactgttgca gatagaagaa Ala Met *			3932
gaggtggttt ctgctcatgt agatctataa atatgtgtt ^g tatgtcttt ttgtttttt tttaaaaaaa agaataactt ttttgcc ^c tc tttagattac atagaagcat tgttagtcttg gtagaaccag tattttgtt gtttat ^t at aaggtattg tgtgtggga aaagtgcagt atttacctgt tgaattcagc atcttgagag cacaaggaa aaaataagaa cctacgaata ttttgagggc agataatgat ctatgttgc ^t tttcttagtta gtgggtttt gaagagggtt ttttat ^t ttttaaaaaa aggttcttaa acattattt ^g aaatagtta ^a tataaatac ^a taattgcatt tgctctgttt attgtatgtt attctaaatt aatgcagaac catatggaa atttcattaa aatctatccc caaatgtgtt ttctgttatcc ttcccttctac ctattattct gatttttaaa aatgcagttt aatgtaccatt tatttgcttg atgaaggag ctctattttc			3992 4052 4112 4172 4232 4292 4352 4412 4472

tttaccagaa atgttgctaa gtaattccca atagaaaagct gcttatttc attaatgaaa	4532
aataaccatg gtttgatac tagaagtctt cttcagaaac tggtgaggct ttctgttcaa	4592
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<211> 1064

<212> PRT

<213> Homo Sapiens

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Val Glu Pro Lys Thr Ala Leu Pro Phe Asn Arg Phe Leu Pro Asn Lys	
20 25 30	
Ser Arg Gln Pro Ser Tyr Val Pro Ala Pro Leu Arg Lys Lys Lys Pro	
35 40 45	
Asp Lys His Glu Asp Asn Arg Arg Ser Trp Ala Ser Pro Val Tyr Thr	
50 55 60	
Glu Ala Asp Gly Thr Phe Ser Arg Leu Phe Gln Lys Ile Tyr Gly Glu	
65 70 75 80	
Asn Gly Ser Lys Ser Met Ser Asp Val Ser Ala Glu Asp Val Gln Asn	
85 90 95	
Leu Arg Gln Leu Arg Tyr Glu Glu Met Gln Lys Ile Lys Ser Gln Leu	
100 105 110	
Lys Glu Gln Asp Gln Lys Trp Gln Asp Asp Leu Ala Lys Trp Lys Asp	
115 120 125	
Arg Arg Lys Ser Tyr Thr Ser Asp Leu Gln Lys Lys Glu Glu Arg	
130 135 140	
Glu Glu Ile Glu Lys Gln Ala Leu Glu Lys Ser Lys Arg Ser Ser Lys	
145 150 155 160	
Thr Phe Lys Glu Met Leu Gln Asp Arg Glu Ser Gln Asn Gln Lys Ser	
165 170 175	
Thr Val Pro Ser Arg Arg Met Tyr Ser Phe Asp Asp Val Leu Glu	
180 185 190	
Glu Gly Lys Arg Pro Pro Thr Met Thr Val Ser Glu Ala Ser Tyr Gln	
195 200 205	
Ser Glu Arg Val Glu Glu Lys Gly Ala Thr Tyr Pro Ser Glu Ile Pro	
210 215 220	
Lys Glu Asp Ser Thr Thr Phe Ala Lys Arg Glu Asp Arg Val Thr Thr	
225 230 235 240	
Glu Ile Gln Leu Pro Ser Gln Ser Pro Val Glu Glu Gln Ser Pro Ala	
245 250 255	
Ser Leu Ser Ser Leu Arg Ser Arg Ser Thr Gln Met Glu Ser Thr Arg	
260 265 270	
Val Ser Ala Ser Leu Pro Arg Ser Tyr Arg Lys Thr Asp Thr Val Arg	
275 280 285	
Leu Thr Ser Val Val Thr Pro Arg Pro Phe Gly Ser Gln Thr Arg Gly	
290 295 300	
Ile Ser Ser Leu Pro Arg Ser Tyr Thr Met Asp Asp Ala Trp Lys Tyr	
305 310 315 320	
Asn Gly Asp Val Glu Asp Ile Lys Arg Thr Pro Asn Asn Val Val Ser	

325	330	335
Thr Pro Ala Pro Ser Pro Asp Ala Ser Gln Leu Ala Ser Ser		
340	345	350
Ser Gln Lys Glu Val Ala Ala Thr Glu Glu Asp Val Thr Arg	Leu Pro	
355	360	365
Ser Pro Thr Ser Pro Phe Ser Ser Leu Ser Gln Asp Gln Ala Ala	Thr	
370	375	380
Ser Lys Ala Thr Leu Ser Ser Thr Ser Gly Leu Asp Leu Met Ser	Glu	
385	390	395
Ser Gly Glu Gly Glu Ile Ser Pro Gln Arg Glu Val Ser Arg Ser	Gln	
405	410	415
Asp Gln Phe Ser Asp Met Arg Ile Ser Ile Asn Gln Thr Pro	Gly Lys	
420	425	430
Ser Leu Asp Phe Gly Phe Thr Ile Lys Trp Asp Ile Pro	Gly Ile Phe	
435	440	445
Val Ala Ser Val Glu Ala Gly Ser Pro Ala Glu Phe Ser Gln	Leu Gln	
450	455	460
Val Asp Asp Glu Ile Ile-Ala Ile Asn Asn Thr Lys Phe Ser	Tyr Asn	
465	470	475
Asp Ser Lys Glu Trp Glu Glu Ala Met Ala-Lys Ala Gln Glu	Thr Gly	
485	490	495
His Leu Val Met Asp Val Arg Arg Tyr Gly Lys Ala Gly Ser	Pro Glu	
500	505	510
Thr Lys Trp Ile Asp Ala Thr Ser Gly Ile Tyr Asn Ser	Glu Lys Ser	
515	520	525
Ser Asn Leu Ser Val Thr Thr Asp Phe Ser Glu Ser Leu Gln	Ser Ser	
530	535	540
Asn Ile Glu Ser Lys Glu Ile Asn Gly Ile His Asp Glu Ser	Asn Ala	
545	550	555
Phe Glu Ser Lys Ala Ser Glu Ser Ile Ser Leu Lys Asn Leu	Lys Arg	
565	570	575
Arg Ser Gln Phe Phe Glu Gln Gly Ser Ser Asp Ser Val Val	Pro Asp	
580	585	590
Leu Pro Val Pro Thr Ile Ser Ala Pro Ser Arg Trp Val	Trp Asp Gln	
595	600	605
Glu Glu Glu Arg Lys Arg Gln Glu Arg Trp Gln Lys Glu	Gln Asp Arg	
610	615	620
Leu Leu Gln Glu Lys Tyr Gln Arg Glu Gln Glu Lys Leu Arg	Glu Glu	
625	630	635
Trp Gln Arg Ala Lys Gln Glu Ala Glu Arg Glu Asn Ser	Lys Tyr Leu	
645	650	655
Asp Glu Glu Leu Met Val Leu Ser Ser Asn Ser Met Ser	Leu Thr Thr	
660	665	670
Arg Glu Pro Ser Leu Ala Thr Trp Glu Ala Thr Trp Ser	Glu Gly Ser	
675	680	685
Lys Ser Ser Asp Arg Glu Gly Thr Arg Ala Gly Glu Glu	Glu Arg Arg	
690	695	700
Gln Pro Gln Glu Glu Val Val His Glu Asp Gln Gly Lys	Lys Pro Gln	
705	710	715
Asp Gln Leu Val Ile Glu Arg Glu Arg Lys Trp Glu Gln Gln	Leu Gln	
725	730	735

Glu Glu Gln Glu Gln Lys Arg Leu Gln Ala Glu Ala Glu Gln Lys
 740 745 750
 Arg Pro Ala Glu Glu Gln Lys Arg Gln Ala Glu Ile Glu Arg Glu Thr
 755 760 765
 Ser Val Arg Ile Tyr Gln Tyr Arg Arg Pro Val Asp Ser Tyr Asp Ile
 770 775 780
 Pro Lys Thr Glu Glu Ala Ser Ser Gly Phe Leu Pro Gly Asp Arg Asn
 785 790 795 800
 Lys Ser Arg Ser Thr Thr Glu Leu Asp Asp Tyr Ser Thr Asn Lys Asn
 805 810 815
 Gly Asn Asn Lys Tyr Leu Asp Gln Ile Gly Asn Thr Thr Ser Ser Gln
 820 825 830
 Arg Arg Ser Lys Lys Glu Gln Val Pro Ser Gly Ala Glu Leu Glu Arg
 835 840 845
 Gln Gln Ile Leu Gln Glu Met Arg Lys Arg Thr Pro Leu His Asn Asp
 850 855 860
 Asn Ser Trp Ile Arg Gln Arg Ser Ala Ser Val Asn Lys Glu Pro Val
 865 870 875 880
 Ser Leu Pro Gly Ile Met Arg Arg Gly Glu Ser Leu Asp Asn Leu Asp
 885 890 895
 Ser Pro Arg Ser Asn Ser Trp Arg Gln Pro Pro Trp Leu Asn Gln Pro
 900 905 910
 Thr Gly Phe Tyr Ala Ser Ser Val Gln Asp Phe Ser Arg Pro Pro
 915 920 925
 Pro Gln Leu Val Ser Thr Ser Asn Arg Ala Tyr Met Arg Asn Pro Ser
 930 935 940
 Ser Ser Val Pro Pro Pro Ser Ala Gly Ser Val Lys Thr Ser Thr Thr
 945 950 955 960
 Gly Val Ala Thr Thr Gln Ser Pro Thr Pro Arg Ser His Ser Pro Ser
 965 970 975
 Ala Ser Gln Ser Gly Ser Gln Leu Arg Asn Arg Ser Val Ser Gly Lys
 980 985 990
 Arg Ile Cys Ser Tyr Cys Asn Asn Ile Leu Gly Lys Gly Ala Ala Met
 995 1000 1005
 Ile Ile Glu Ser Leu Gly Leu Cys Tyr His Leu His Cys Phe Lys Cys
 1010 1015 1020
 Val Ala Cys Glu Cys Asp Leu Gly Gly Ser Ser Ser Gly Ala Glu Val
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 1045 1050 1055
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 <211> 549
 <212> DNA
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 aagctgctcc tctgatatca cgttgagagg ggggcgtgaa gttttgaaa gtgacacaga

60
120

ttcggaaattt acatccaaga tgcaggatta taataaagat gatatgtcgt atcgaaggat	180
ttcggctgtt gagccaaaga ctgcgttacc cttcaatcgt tttttaccca acaaaaagtag	240
acagccatcc tatgtaccag cacctctgag aaagaaaaag ccagacaaac atgaggataa	300
cagaagaagt tggcaagcc cggttatac agaagcagat ggaacatTTT caagactctt	360
tcaaaagatt tatggtgaga atgggagtaa gtccatgagt gatgtcagcg cagaagatgt	420
tcaaaacttg cgtcagctgc gttacgagga gatgcagaaa ataaaatcac aattaaaaga	480
acaagatcag aaatggcagg atgaccttgc aaagtggaaa gatcgtcgaa aaagttacac	540
ttcagatct	549

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<220>
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gtAACTTTT cgacgatctt tccac 25

<210> 7
<211> 25
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<220>
<223> Primer

<400> 7
tatTTTCTGC atctcctcgt aacgc 25

<210> 8
<211> 25
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<220>
<223> Primer

<400> 8
tgacatcaCT catggactta ctccc 25

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<400> 9

gttccatctg cttctgtata aaccg 25

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<212> DNA
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<220>
<223> Primer

<400> 18
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<210> 19

<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 19
ggtgaaccag cctttccata gc

22